Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1 (previously presented): In a method of providing a mixture of DNA fragments enriched in fragments that are characteristic of a phenotype of interest, which method includes providing affected DNA in fragmented form and providing unaffected DNA in fragmented form, the improvement comprising:

a) mixing the fragments of the affected DNA and the fragments of the unaffected DNA under hybridising conditions to form hybrids;

b) recovering a mixture of hybrids that contain mismatches;

c) recovering fragments of the affected DNA from the mixture of hybrids that contain mismatches.

Claim 2 (currently amended): The method of claim 1, wherein the affected DNA is pooled DNA of one or more individuals who show the phenotype of interest, and the

unaffected DNA is pooled DNA of one or more individuals who do not show the phenotype of interest.

Claim 3 (canceled)

Claim 4 (original): The method of claim 1, wherein the affected DNA is DNA of one individual who shows the phenotype of interest, and the unaffected DNA is pooled DNA of a complete set of ancestors who do not show the phenotype of interest.

Claim 5 (original): The method of claim 1, wherein the affected DNA is DNA from cells of an individual that show the phenotype of interest, and the unaffected DNA is DNA from cells of the individual that do not show the phenotype of interest.

Claim 6 (previously presented): The method of claim 1, wherein step b) is performed by use of a mismatch-binding protein.

Claim 7 (previously presented): The method of claim 1, wherein either the fragments of the affected DNA or the fragments of the unaffected DNA are tagged by one member of a specific binding pair, and step c) is performed by using the other member of the specific binding pair.

Claim 8 (original): The method of claim 7, wherein the fragments of the unaffected DNA are tagged with biotin, and step c) is performed by use of immobilised streptavidin.

Claim 9 (previously presented): The method of claim 1, further comprising subjecting the mixture of DNA fragments enriched in fragments that are characteristic of the phenotype of interest to self-hybridisation to form duplexes and subsequently recovering the perfectly matched duplexes.

Claim 10 (previously presented): The method of claim 1, further comprising mixing the mixture of DNA fragments enriched in fragments that are characteristic of the phenotype of interest with an excess of the fragments of the affected DNA under hybridisation conditions to form duplexes and subsequently recovering the perfectly matched duplexes.

Claim 11 (previously presented): The method of claim 1, wherein each of the affected DNA and the unaffected DNA is provided in fragmented form by digestion with from 4 to 7 six-cutter restriction endonuclease enzymes together with from 0 to 50 four-cutter restriction endonuclease enzymes.

Claims 12–13 (canceled)

Claim 14 (original): A method of making a set of arrays of fragments of DNA of interest, which method comprises;

a) selecting, from a set of n restriction endonuclease enzymes, a subset of r restriction endonuclease enzymes;

b) digesting genomic DNA with the subset of r enzymes;

c) ligating to the resulting fragments restriction-enzyme-cutting-site-specific adapters with unique polymerase chain reaction amplifiable sequences;

d) splitting the resulting fragments into r^2 aliquots;

e) amplifying each aliquot with two restriction-enzyme-specific primers;

f) forming an array of the r^2 aliquots of non-tagged amplimer strands; and

g) repeating steps a) to f) using one or more different subsets of r restriction endonuclease enzymes.

Claim 15 (currently amended): The method of claim 14, wherein steps ~~a~~ a) to f) are repeated using each different subset of r restriction endonuclease enzymes to give (n!)/[(n-r)!r!] different arrays.

Claim 16 (currently amended): The method of claim 14, wherein the n restriction endonuclease enzymes are selected from ~~4-cutters and 5-cutters~~the group consisting of 4-cutters, 5-cutters and 6-cutters.

Claim 17 (previously presented): The method of claim 14, wherein the n is 3 to 10 and r is 2 to 4.

Claim 18 (original): The method of claim 17, wherein n = 6 and r = 3.

Claim 19–20 (canceled)

Claim 21 (previously presented): A set of arrays produced by the method of claim 14, derived from a set of n = 6 six-cutter restriction endonuclease enzymes which are *BamHI*; *Bsr GI*; *Hind III*; *Ncol*; *Spel*; and *AflII*.

Claim 22 (previously presented): A set of arrays produced by the method of claim 14, derived from the set of n = 6 six-cutter restriction endonuclease enzymes which are *EcoRI*; *BspHI*; *BglII*; *Xbal*; *Acc65I*; and *ApaLI*.

Claim 23 (previously presented): A nucleic acid characterisation method which comprises presenting to a set of arrays produced by the method of claim 14 a nucleic acid fragment of interest under hybridisation conditions, and observing a pattern of hybridisation.

Claim 24 (original): The method of claim 23, wherein a plurality of nucleic acid fragments of interest are separately presented to the set of arrays, and the resulting patterns of hybridisation are compared.

Claim 25 (original): The method of claim 24, wherein the plurality of nucleic acid fragments of interest are drawn from the mixture of DNA fragments, enriched in fragments that are characteristic of a phenotype of interest, of claim 13.

Claim 26 (canceled)

Claim 27 (currently amended): A double-stranded DNA molecule having the sequence a-A-b-B...X-y-Y-z where A, B...X and Y are unique restriction sites for n different restriction endonuclease enzymes, and a, b...y, z denotes distances in base pairs, ~~characterised in that~~wherein each fragment, obtainable by cutting the DNA molecule by

means of any one or more up to n of the restriction enzymes, has a different length from every other fragment.

Claim 28 (previously presented): The double-stranded DNA molecule of claim 27, wherein:

a) inter-fragment length differences are greater for larger fragments;

b) all possible fragments are unambiguously resolvable by electrophoresis from one another;

c) size gaps between bands comprising different numbers of inter-restriction-site units are larger than size gaps between bands comprising the same number of inter-restriction-site units;

d) the size gaps and size spread from the largest to the smallest fragment are electrophorectically compatible.

Claim 29 (currently amended): The method of claim 1, which further comprises performing steps a), b) and c) one or more times.

Claim 30 (currently amended): The method of claim 14, wherein one of the restriction enzyme specific primers is tagged.